



DNA sequence:

cccttcattgtctttttagtagaaacccccattatcttttcttagggcccaattgaaaacccacattttctttcacctaacc
ccaaagccttgcacatgttgacgtgaacaccaaactaacacgtgtcatactgccagtggttatgataaatgctcatacc
ataccagagtcataagagtttttggttggtgaaagatttgacggatgccttctctcatttctcaccacactccctccaaa
cccaacaaaatgtttatattagcaaaagccgcaaaagtgtaaacgaaagtttataaatttcatttctgtgatcttacgta
attgggaggaagatcaaaattttcaatccccattctctcgattgcttcaattgaagtttctccg

[transit peptide start]

ATGGCGCAAGTTAGCAGAATCTGCAATGGTGTGAGAACCCTCTCTTATCTCCAATCTCTCGAAATCCAGTCAACGCA
AATCTCCCTTATCGGTTTCTCTGAAGACGCAGCAGCATCCACGAGCTTATCCGATTTCTGTCGTCGTTGGGGATTGAAGAA
GAGTGGGATGACGTTAATTGGCTCTGAGCTTCGTCCTCTTAAGGTCATGTCTTCTGTTTCCACGGCGGAG

[mature peptide starts]

AAAGCGTCGAGATTGTACTTCAACCCATTAGAGAAATCTCCGGTCTTATTAAGCTTCTGGCTCCAAGTCTCTATCAA
ATCGGATCTGCTTCTCGCTGCTCTGTCTGAGGTATATATCACTTCGTTTCGTCCTTCTCTGTAATCTGAACCTTAGATT
ATAAAGATTGATACTTTACCATTTTGTCTGTGGTTTATAGGGAACAACCTGTAGTGGACAACCTTGTGAATAGCGATGAC
ATCAATTACATGCTTGATGCGTTGAAGAGATTGGGACTTAATGTGGAACTGACAGTGAAAATAATCGTGCTGTAGTTG
AAGGATGTGGCGGGATATTTCCAGCTTCCATAGATTCAAAGAGTGATATCGAACTTTACCTCGGTAATGCAGGAACAGC
AATGCGTCCAATTACCGCTGCGGTCACTGCTGCAGGTGGAAACGCAAGGTAGATTGAAGGAGTTGATGCTTCTTGGTAT
TTGATGTTTAAAGGAATGGAGCTTTTGTGATGCTTTATGATCCATTTATCCAGTTATGTGCTTGATGGGGTGCCTCGT
ATGAGAGAAAGACCTATAGGGGATTGGTTGTTGGTCTTAAGCAGCTTGGTGCTGATGTTGAATGTAATCTTGGAACTA
ACTGCCCTCCTGTTTCGTGTCAACGCTAATGGTGGCCTTCCCGGTGGAAAGGTTAGATCTTGCAATGGCATGTGAATAT
GTAATCTCGTTCCTTACTCTATGAACACTTGCAGAAATGTGTGTTTATCATAGCCTTAGCTTGACAAGATTTTCACTTTT
TAATCTACTCTCAACGGATGGATCCTAAAATAGAATCGGATTTGGTGATTGGTTTTCTGTTCTCGATTACCGTTTTCTGTT
GTATGATTTCTTGATTAACAATTAGGAGACATGTTATGCATTTGCAGGTGAAGCTTTCTGGATCAATTAGTAGTCAGTA
CTTGACTGCTCTGCTCATGTCTGCTCCCTTAGCTCTTGGAGACGTCGAGATTGAGATTGTGATAAATTAATTTCTGTT
CCATATGTTGAAATGACATTGAAGTTGATGGAACGTTTCCGGGTTAGTGTGAGCATAGTGATAGCTGGGATCGTTTCT
TTGTCAAGGGCGGGCAAAAATACAAGTAGGAGTTATTCTTTCTTCTTCTTCTGAAATCACATCCCTTAGCTTGACAAT
ATAATGACTAAAAGGTGAATGATTCAAGGTCTCCGGGTAATGCGTATGTAGAAGGTGATGCTTCTAGTGCATGTTATTTT
TTGGCTGGTGCTGCCATTACCGGTGAAACTGTCAAGTCAGTCGAAGGTTGTGGAACCTACCAGCTTGCAAGGTAATTTGTAC
ACTGAATCATCGACGAGGCTGTTAAGTTTATAGTGAAATTCGTCTAGGTCAAAGTTTCTATCTTTTGACAAGTTGTATAT
AACATATTGCAAGATTCTAAGCTCAATTTTTGTGATGAATCTCTAGGGAGATGTAAAATTCGCCGAGGTCCTTGAGAA
AATGGGATGTAAAGTGTCTGGACAGAGAACAGTGTGACTGTGACAGGACCACCTAGAGATGCTTTTGGAATGAGACAC
TTGCGGGCTATTGATGTCAACATGAACAAAATGCCTGATGTAGCCATGACCCTTGCCGTGCTTGTCTCTTTGCTGACG
GTCCAACCACCATTAGAGATGGTAAGTAAAAAGCTCTCTCTTATAAATTAAAGGTTTCTCAATATTCATGATCACTTAATT
CTGTTTGGTTAATATAGTGGCTAGCTGGAGAGTAAAGGAGACAGAAAGGATGATTGCCATTTGCACAGAGCTTAGAAAA
GTAAGAGATTCTTATCTCTCTCTTCTGTCTCTTGACAGTGCTCATTCTAAGTAATTAGCTCATAAATTTGTGTGTTT
TGTTCAAGTGGGAGCTACAGTGGAAGAAGGTTCAAGATTATGTGTGATAACTCCGCCAAAAAGGTGAAAACGGCAGAG
ATTGATACATATGATGATCATAGAATGGCAATGGCATTCTCTTGCAGCTTGTGCTGATGTTCCAATCACCATCAACG
ACTCTGGTTGCACAGGAAAACCTTCCCCGACTACTTCCAAGTACTTGAAAGAATCACAAGCACTAAacataaactc
tgttttttcttctctgatccaagctt

Fig. 1A



Protein sequence:

MAQVSRICNGVQNPSLISNLSKSSQKSPLSVLKTQHPRAYPISSSWGKKSGMTLIGSELRLPKVMSSVSTAE
KASEIVLQPIREISGLIKLPGSKSLSNRIILLIAALSEGTTVDNLLNSDDINYMLDALKRGLGNVETDSENNRAVV
EGCGGIFPASIDSKSDIELYLGNAGTAMPELTAAVTAAGNASYVLDGVPRMRERPIGDLVVGLKQLGADVETLG
TNCPPVRVNANGGLPGGKVKLSGSISSQYLTALLMSAPLALGDVEIEIVDKLISVPYVEMTLKLMERFGVSVEHSD
SWDRFFVKGQKYKSPGNAYVEGDASSACYFLAGAAITGETTVVEGCGTTSLQGDVKFAEVLEKMGCKVSWTENS
TVTGPPRDAFGMRHLRAIDVNMNKMPPDVAMTLAVVALFADGPTTIRDVASWRVKETERMIAICTELRKL
SDYCVITPPKKVKTAETIDYDDHRMAMAFSLAACADVPIITINDSGCTRKTFFPDYFQVLERITKH

Fig. 1B



Arabidopsis thaliana wild type sequence:

| | | | | | | | | | | | |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Position | 173 | 174 | 175 | 176 | 177 | 178 | 179 | 180 | 181 | 182 | 183 |
| | L | G | N | A | G | T | A | M | R | P | L |
| | CTC | GGT | AAT | GCA | GGA | ACA | GCA | ATG | CGT | CCA | CTT |

Arabidopsis thaliana mutant sequences:

| | | | | | | | | | | | | |
|--|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Name | | CTC | GGT | AAT | GCA | GCA | ACA | GCA | ATG | CGT | CCA | CTT |
| A ₁₇₇ | | L | G | N | A | A | T | A | M | R | P | L |
| I ₁₇₈ | | CTC | GGT | AAT | GCA | GGA | ATA | GCA | ATG | CGT | CCA | CTT |
| | | L | G | N | A | I | T | A | M | R | P | L |
| A ₁₇₇ I ₁₇₈ | | CTC | GGT | AAT | GCA | GCA | ATA | GCA | ATG | CGT | CCA | CTT |
| | | L | G | N | A | A | I | A | M | R | P | L |
| I ₁₇₈ S ₁₈₂ | | CTC | GGT | AAT | GCA | GGA | ATA | GCA | ATG | CGT | TCA | CTT |
| | | L | G | N | A | G | I | A | M | R | S | L |
| A ₁₇₇ S ₁₈₂ | | CTC | GGT | AAT | GCA | GCA | ACA | GCA | ATG | CGT | TCA | CTT |
| | | L | G | N | A | A | T | A | M | R | S | L |
| A ₁₇₇ I ₁₇₈ S ₁₈₂ | | CTC | GGT | AAT | GCA | GCA | ATA | GCA | ATG | CGT | TCA | CTT |
| | | L | G | N | A | A | I | A | M | R | S | L |
| V ₁₇₈ S ₁₈₂ | | CTC | GGT | AAT | GCA | GGA | GTA | GCA | ATG | CGT | TCA | CTT |
| | | L | G | N | A | G | V | A | M | R | S | L |
| L ₁₇₈ S ₁₈₂ | | CTC | GGT | AAT | GCA | GGA | TTA | GCA | ATG | CGT | TCA | CTT |
| | | L | G | N | A | G | L | A | M | R | S | L |
| A ₁₇₇ V ₁₇₈ | | CTC | GGT | AAT | GCA | GCA | GTA | GCA | ATG | CGT | CCA | CTT |
| | | L | G | N | A | A | V | A | M | R | P | L |
| A ₁₇₇ L ₁₇₈ | | CTC | GGT | AAT | GCA | GCA | TTA | GCA | ATG | CGT | CCA | CTT |
| | | L | G | N | A | A | L | A | M | R | P | L |

Fig. 2

100
(1) ATGGCGCAAGTTAGCAGAATCTGCAATGGTGTGCGAAGCCCAT---CTCTTATCTCCAATCTCTCGAATCCAGTCAACGCAAAATCTCC---CTTATCGG
(1) ATGGCGCAATCTAGCAGAATCTGCAATGGTGTGCGAAGCCCATCTGTTATCATCTCCAATCTCTCCAATCTCTCCAATCCAAACCAAAATCACC---TTTCTCCG
(1) ATGGCACAATTAAACAACATGGCTCAAGGGATACAAACCTTA---ATCCCAATTCCAATTTCCATAAACCCCAAGTTCCCTAAATCTTCAAGTTTCTTG
(1) GCGG-----
101
(95) TTTCT---CTGAAGACGACGAGCATCCACGAGCTTATCCGATTTCTGTCGTGGGATTTGAAGAAGAGTGGGATGAAGTTAATTGGCTCTGAGCTTCG
(98) TCTCC---TTGAAGACGACATCAGC---CTCGAGCTT-----CTTCGTGGGATTTGAAGAAGAGTGGAAGATGCTAAACCGTTCTGTAAATTCG
(98) TTTTGGATCTAAAAAACTGAAAAATTCAGCAAAAT---CTATGTTGGT---TGAAAAAAGATTCAAATTT---TATGCAAAAGTTTGT
(5) -----GTCCCGAGG-----
200
(192) TCCTCTTAAGGTCATGTCCTTCTGTTTCCACGCGCGAGAAAGCTCGGAGATTGTACTTCAACCCATTAGAGAAATCTCCGGTCTTATTAAGTTCCTGGC
(180) CCGGTTAAGGTAAACAGTTCTGTTTCCACGCTCGAGAAAGCTTCAGAGATTGTGCTTCAACCAATCAGAGAAATCTCGGTCTCATTAAGCTACCCGGA
(180) TTCCTTTAGGATTTTACGATCAGTGGCTACAGCAGAGCCCTCTGAGATAGTGTGCAACCCATTAAAGAGATTTTCAGGCACCTGTTAAATTCCTGGC
(14) -----AGATCGTGTGTCAGCCCATCAAGGAGATCTCCGGCACCGTCAAGCTGCGGGG
300
(292) TCCAGTCTCTATCAAAATCGGATCCTGCTTCTCGTCTCTGAGGAAACAACTGTAGTGGACAACTTGTGTAATAGCGATGACATCAATACATGC
(280) TCCAAATCTCTCCAATCGGATCCTCTTCTGCGCTCTATCTGAGGAACTACTGTAGTGACAACTTGTGGAACAGTGTGATGACATCAACTACATGC
(280) TCTAAATCAATATCTAATAGAAATCTCTTCTGCTGCTTATCTGAAGAAACAACTGTGTTGACAAATTACTAAGTAGTATGATTCATTAACATGC
(67) TCCAGTGCCTTTCCAAACCGGATCCTCTACTCGCCGCCCTGTCCGAGGGGACAACTGTGTTGATAACCTGCTGAACAGTGAAGATGTCCACTACATGC
400
(392) TTGATGCGTTGAAGAGATTGGACTTAATGTGAAACGTGACAGTGAATAATCGTGTGTAGTTGAAGATGTGGGGGATATCCAGCTTCCATAGA
(380) TTGATGCGTTGAAGAGTTGGGCTTAAACGTGAAACGTGACAGTGAATAACCAACCGTGGTGTGTTGAAGATGTGGGGGATATCCAGCTTCCATAGA
(380) TTGATGCGTTGAAACCACTTGGACTGCACTGTAAGAGATAGTGAACCAACCGAGTGTGTTGAAGTGTGGGGGCTTTCCCTGTTGGTAAAGA
(167) TCGGGGCTTGAAGACTCTTGGTCTCTCTGTCGAAGCGGACAAAGCTGCCAAAGAGCTGTAGTTGCTGTGGTGTGGAAAGTTCCAGATTG---AGGA
500
(492) TTCAAAGAGTGATATCGAACTTTTACCTCGGTAATGCAGAAACAGCAATGCGTCCACTTACCGTGGTCACTGTGTCAGGTGGAAACCGCAAGTTATGTG
(480) TTCAAAGAGTGATATTCAGTTGTAGTTGGAATGCAAGAAACAGCAATGCGTCCACTTACCGTGGTCACTGTGTCAGGTGGGCAACCGCAGTTATGTA
(480) GTCAAAGGAAGAAATTCATCTGTTCTTGGAAATGCAAGAAACAGCAATGCGGCCCACTAACAGCAGCAGTTACTGTAGCTGGTGGAAATTCAGAGTATGTA
(264) TGCTAAAGAGGAAGTGACGCTCTTCTTGGGGAATGCTGAACTGCAATGCGGCCCACTGACAGCAGCTGTACTGCTGCTGTGGTGGAAATGCAACTTACGTC
600

Fig. 3A



Non-Transgenic Herbicide
Resistant Plant
Peter R. Beetham et al.
Serial No. 09/685,403

601
(592) atepspscDNA.seq
(580) bnepsdcna.seq
(580) petaroacdna.seq
(364) zmepps.seq
700
(692) atepspscDNA.seq
(680) bnepsdcna.seq
(680) petaroacdna.seq
(464) zmepps.seq
800
(792) atepspscDNA.seq
(780) bnepsdcna.seq
(780) petaroacdna.seq
(564) zmepps.seq
900
(892) atepspscDNA.seq
(880) bnepsdcna.seq
(880) petaroacdna.seq
(664) zmepps.seq
1000
(992) atepspscDNA.seq
(980) bnepsdcna.seq
(980) petaroacdna.seq
(764) zmepps.seq
1100
(1092) atepspscDNA.seq
(1080) bnepsdcna.seq
(1080) petaroacdna.seq
(864) zmepps.seq

Fig. 3B



| | |
|------------------|---|
| 1201 | 1300 |
| atepspscDNA. seq | (1192) ATTGATGTCAACATGAACAAAATGCGCTGATGTAGCCATGACCCCTTGCGCTGTTGCTCTCTTTGCTGACGGTCCAAACCATTAGAGATGTGGCTAGCT |
| bnepscdna. seq | (1180) GTTGATGTCAACATGAACAAAATGCGCTGATGTAGCCATGACCTTAGCCGTTGTTGCTCTCTTTGCGGATGGTCCAAACCATCAGAGATGTGGCTAGCT |
| petaroacdna. seq | (1180) ATTGATGTGAACATGAATAAAATGCGCTGATGTAGCCATGACACTTGTCTGTTGCTGCTGATGTTGCACTTTATGCTGATGGTCCACAGCTATATAAGAGATGTTGCTAGCT |
| zmepsps. seq | (964) ATTGATGTCAACATGAACAAAGATGCGCTGATGTAGCCATGACTCTTGTCTGTGTTGCCCTCTTTGCGGATGGCCGACAGCCATCAGAGACGTGGCTTCCCT |
| 1301 | 1400 |
| atepspscDNA. seq | (1292) GGAGAGTAAAGGAGACAGAAAGGATGATTGCCATTTGCACAGAGCTTAGAAAACTGGGAGCTACAGTGGAAAGAAAGTTTCAGATTATTGTGTGATAACTCC |
| bnepscdna. seq | (1280) GGAGAGTTAAGGAGACAGAGAGGATGATTGCCATTTGCACAGAGCTTAGAAAACTGGGAGCTACAGTGGAAAGAAAGTTTCAGATTATTGTGTGATAACTCC |
| petaroacdna. seq | (1280) GGAGAGTCAAGGAAACTGAGCGCATGATCGCCATATGCAAGAACTTAGAAAGTTAGGAGCAACCGTTGAAAGAACGACTACTGCATAATCACCCCC |
| zmepsps. seq | (1064) GGAGAGTAAAGGAGACCGAGAGGATGGTTGGGATCCGACGGAGCTAACCAAGCTGGGAGCATCTGTTGAGGAAGGGCCCGGACTACTGCATCATCAGCCC |
| 1401 | 1500 |
| atepspscDNA. seq | (1392) GCCCAAAAAGGTGAAAACCGCAGAGATTGATACATATGATGATCATAGAAATGGCAATGGCATTTCTCTTTGCAGCTTGTGCTGATGTTCCCAATCACCATC |
| bnepscdna. seq | (1380) ACCAGCAAAGGTGAAAACCGCGGAGATTGATACGATGATGATCATAGAAATGGCGTTCTCGCTTGCGCTTGTGCTGATGTTCCAGTCAACCATC |
| petaroacdna. seq | (1380) ACCGAGAAACTAAATGTGACCGATATTGATACATACGATGATCACAGGATGGCCATGGCTTTTCTCTGCTGCTGTCAGATGTTCCCGTCAACCATC |
| zmepsps. seq | (1164) GCCGAGAAAGCTGAACCGTGACGGGATCGACACGTCAGACGACCAAGGATGGCCATTTCTCCCTTGTCCGAGGTCCCGGAGGTCCCGCTCAACCATC |
| 1501 | 1572 |
| atepspscDNA. seq | (1492) AACGACTCTGTTGCAACCAAGGAAACCTTCCCGACTACTTCCAAAGTACTTGAAGAATCACAAGGCACTAA |
| bnepscdna. seq | (1480) AAGGATCCTGGCTGCACCAAGGAAAGACTTTCCCTGACTACTTCCAAAGTCTTGAAGTATCACAAGCATTA |
| petaroacdna. seq | (1480) AATGACCTGGCTGCACCGGAAACCTTCCCTAACTACTTTGATGTACTTTCAGCAGTACTTCCAAAGCATTA |
| zmepsps. seq | (1264) CCGGACCTGGGTGCACCCGGAAGACCTTCCCGACTACTTCCGATGTGCTGAGCACTTTTCGTCAAGAAATTA |

Fig. 3C

100
1 MAQVSRICNGVQNP-SLISNLSKSSQKSPLSVSLKTQHPRAYPISSSWGLKSGMTLIGSELR-----PLKVMSSVSTAESAIEIVLQPIREISGLI
(1) MAQSSRICHGQVQPCVVIISNLSKSNQKSPFVSLKTHQ-----PRASSWGLKSGMTLNGSVIR-----PVKVTASVSTSEKASEIVLQPIREISGLI
(1) MAQINNMAQIQITL-NPNSPHKQVPKSSSFLVFGSKK-----LKNSA-----NSMLVLKSDSIFMQKFCFSFRISASVATAQKSEIVLQPIKEISGTV
(1) AG-----AEEIVLQPIKEISGTV

200
101
(94) KLPGSKSLSNRIILLLAALSEGTTVVNDLLNSDDINYMMLDALKRLGLNVETDSENNRAVVEGCGGIPFASIDSKSDIELYLGNAQTAMRPLTAAVTAAGN
(90) KLPGSKSLSNRIILLLAALSEGTTVVNDLLNSDDINYMMLDALKRLGLNVERDSVNNRAVVEGCGGIPFASIDSKSDIELYLGNAQTAMRPLTAAVTAAGN
(90) KLPGSKSLSNRIILLLAALSEGTTVVNDLLNSDDINYMMLDALKRLGLNVERDSVNNRAVVEGCGGIPFASIDSKSDIELYLGNAQTAMRPLTAAVTAAGN
(19) KLPGSKSLSNRIILLLAALSEGTTVVNDLLNSDDINYMMLDALKRLGLNVERDSVNNRAVVEGCGGIPFASIDSKSDIELYLGNAQTAMRPLTAAVTAAGN

300
201
(194) ASYVLDGVPRMRERP IGD LVVGLKQLGADVECTLTGTCPPVRVNVANGGLPGGKVKLSGSISSQYLTALLMSAPLALGDVEIEIIVDKLISVPYVEMTLKLM
(190) ASYVLDGVPRMRERP IGD LVVGLKQLGADVECTLTGTCPPVRVNVANGGLPGGKVKLSGSISSQYLTALLMSAPLALGDVEIEIIVDKLISVPYVEMTLKLM
(190) SRYVLDGVPRMRERP IGD LVVGLKQLGADVECTLTGTCPPVRIVSKGGLPGGKVKLSGSISSQYLTALLMSAPLALGDVEIEIIVDKLISVPYVEMTLKLM
(118) ATYVLDGVPRMRERP IGD LVVGLKQLGADVECTLTGTCPPVRVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIVDKLISVPYVEMTLRLM

400
301
(294) ERFVSVSEHSDSWDRFFVKGQKYSKSPGNAVVEGDASSACVFLAGAAITGETVTVEGCGTSLQGDVKFAEVLKMGCKVSWTENSVTVTGPPRDAFGMR
(290) ERFVSAEHSWDRFFVKGQKYSKSPGNAVVEGDASSASYFLAGAAITGETVTVEGCGTSLQGDVKFAEVLKMGCKVSWTENSVTVTGPPRDAFGMR
(290) ERFVSVSEHSDSWDRFFVKGQKYSKSPGNAFVEGDASSASYFLAGAAITGETVTVEGCGTSLQGDVKFAEVLKMGAEVTTWENSVTVTGPPRDAFGMR
(218) ERFVKAHSWDRFFVKGQKYSKSPNAVVEGDASSASYFLAGAAITGETVTVEGCGTSLQGDVKFAEVLKMGAEVTTWENSVTVTGPPRDAFGMR

500
401
(394) HLRAIDVNMNKMPPDVAMTLAVVALFADGPTTIRDVASWRVKETERMTAICTELRKLGAATVEEGSDYCVITPPKKVKTAEIDTYDDHRMAMAFSLAACADV
(390) HLRAIDVNMNKMPPDVAMTLAVVALFADGPTTIRDVASWRVKETERMTAICTELRKLGAATVEEGSDYCVITPPKKVKTAEIDTYDDHRMAMAFSLAACADV
(390) HLRAIDVNMNKMPPDVAMTLAVVALFADGPTTIRDVASWRVKETERMTAICTELRKLGAATVEEGSDYCVITPPKKVKTAEIDTYDDHRMAMAFSLAACADV
(318) HLRAIDVNMNKMPPDVAMTLAVVALFADGPTTIRDVASWRVKETERMTAICTELRKLGAATVEEGSDYCVITPPKKVKTAEIDTYDDHRMAMAFSLAACADV

501
527
(494) PITINDSGCTRKTFPDYFQVLEIRITKH
(490) PVTIKDPCGCTRKTFPDYFQVLESITKH
(490) PVTINDPGCTRKTFPNYFDVLQOYSKH
(418) PVTIRDPGCTRKTFPDYFDVLSTFVKH

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bnepsps. PRO
petar. PRO
zmepps. PRO

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Fig. 4